

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

1 GTCGACCCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGG  
CAGCTGGGTGCGCAGGCCGTCGTCGGTCCGACGTCGTCGGCTCGTCGTCGTTCTCATTTTCC  
-----  
63 TGACCGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTT  
ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCCGTGTCTACGGTAGGACCTGCGAGAA  
-----  
1 M G R A R D A I L D A L  
-----  
125 GAAAACTTGTGAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG  
CTTTTGAACAGTCCCCTACTTGAGTTTTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC  
-----  
13 E N L S G D E L K K F K M K L L T V Q L R  
-----  
187 AGAAGGCTATGGGCGCATCCACGCGGGGCCCCCTGCTGCAGATGGACGCCATAGATCTCACTG  
TCTTCCGATACCCCGGTAGGGTGCGCCCGGGACGACGTCTACCTGCGGTATCTAGAGTGAC  
-----  
33 E G Y G R I P R G A L L Q M D A I D L T  
-----  
249 ACAAACCTTGTGAGTACTATCTGGAGTCGTATGGCTTGGAGCTCACAATGACTGTGCTTAGA  
TGTTTGAACAGTCGATGATAGACCTCAGCATACCGAACCTCGAGTGTTACTGACACGAATCT  
-----  
54 D K L V S Y Y L E S Y G L E L T M T V L R  
-----  
311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACCGACTAAAGAAGAGTCTGGAGCTGT  
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTTGCTGATTTCTTCTCAGACCTCGACA  
-----  
75 D M G L Q E L A E Q L Q T T K E E S G A V  
-----  
373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTGTGGACCAGC  
CCGTGACGTCGGTCACAGGGACGAGTCTCATGTTCGGTCTTGTCCTGTGAAACACCTGGTCG  
-----  
95 A A A A S V P A Q S T A R T G H F V D Q  
-----  
435 ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGCTGGATGCTTTGTCATGGC  
TGTCGGTTTCGTAGTAACGGTCCAGTGTCTTACCTGCCTCAGGACCTACGAAACGTACCG  
-----  
116 H R Q A L I A R V T E V D G V L D A L H G  
-----  
497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGACCACCAGCCAAGACAAGAT  
TCACACGACTGACTTCCTGTGTCATGGTCCGTCAAGCACGTCTCTGGTGGTCGGTTCTGTTCTA  
-----  
137 S V L T E G Q Y Q A V R A E T T S Q D K M  
-----  
559 GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG  
CTCCTTCGAGAAGTCGAAACAAGGTAGGACCTTGGAAGTGGACGTTCTGAGGGAGGAGGTCC  
-----  
157 R K L F S F V P S W N L T C K D S L L Q  
-----  
621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC  
GGAACCTCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG (SEQ ID NO:3)  
-----  
178 A L K E I H P Y L V M D L E Q S (SEQ ID NO:2)  
-----  
683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTTGAAAAACAATTTGTATTTGT  
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTAAAAACTTTTTTGTAAACATAAACA  
-----  
745 GTTTAAAAAAGGGCGGCCGC (SEQ ID NO:1)  
CAAAATTTTTTTTTTTTTTTTTTCCCGCCGGCG  
-----

FIG. 1

Applicant(s): John Bertin

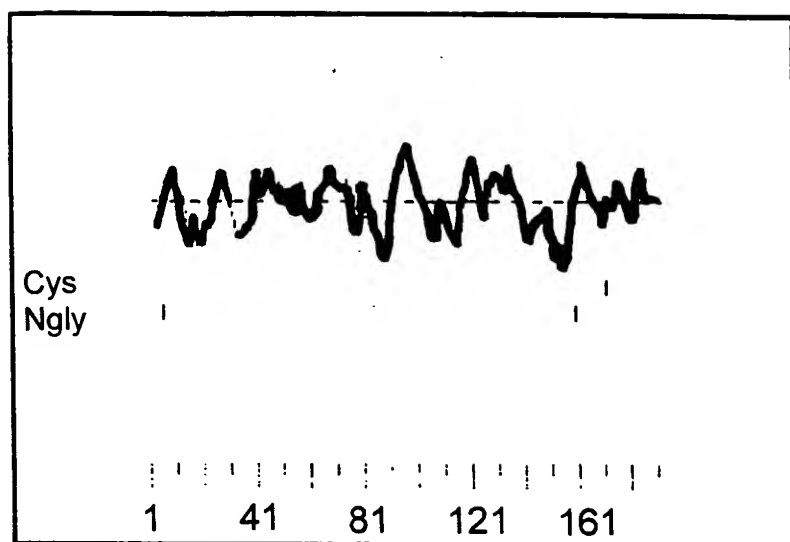
NOVEL MOLECULES OF THE CARD-RELATED PROTEIN  
FAMILY AND USES THEREOF

FIG. 2

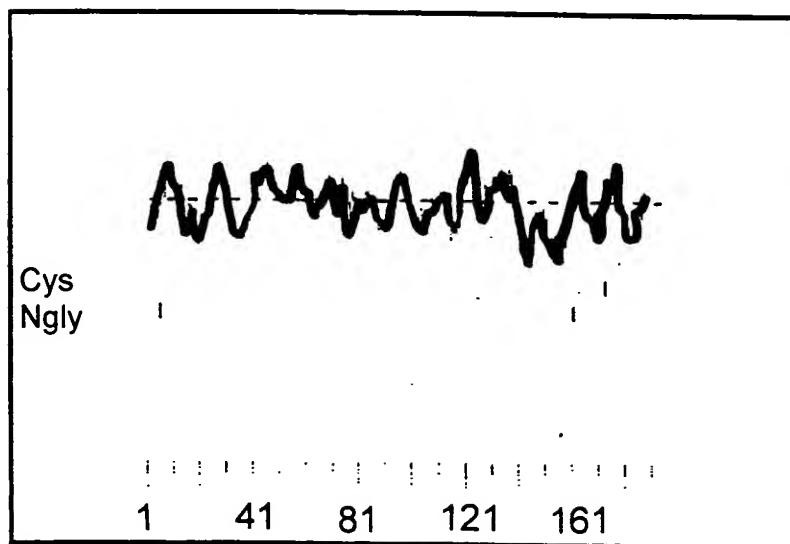


FIG. 4

Applicant(s): John Bertin

NOVEL MOLECULES OF THE CARD-RELATED PROTEIN  
FAMILY AND USES THEREOF

1 CGCGTCCGGCTGCAGCGGGGTGAGCGGCGGCAGCGGCCGGGGATCCTGGAGCCATGGGGC  
GCGCAGGCGCGACGTGCGCCCCACTGCGCGCCGTGCGCGGCCCTAGGACCTCGGTACCCCG  
1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT  
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA  
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTGCGGTGCGGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG  
AGTTGCACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCCGCTAGGGCGCCCCCG  
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCCTTGGACCTCACCGACAAGCTGGTCACTTCTACCTGGAGA  
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTGACCCAGTCAAGATGGACCTCT  
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCG  
GGATGCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGACGTCTCTACCGGC  
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC  
CCGTCGACGTCCGCGGCTGCGTGGTCCCGAGACCTCGCGCGGTCGACCCCTAGGTCCGG  
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA  
GAGGAGTCAGCCGTGCGTTCCGGTCCGGACGTGAAATATCTGGTCTGGCCCCGACGCGAAT  
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCCGAGAGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG  
AGCGCTCCAGTGTTTGCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC  
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCAGGCGGAGCCACCAACCCAAGCAAGATGCGGAAGCTCT  
TACTCGTCATGGTCCGTACGCCCCGGCTCGGGTGGTTGGGTTCTACGCCTTCGAGA  
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTCACACCAGCCTGGAACCTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG  
AGTCAAAGTGTGGTCCGACCTTGACCTGGACGTTCTGAACGAGGAGGTCCGGGATTCCC  
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCCAGCAACAC  
TCAGGGTCAGGATGGACCACCTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG (SEQ ID NO:6)  
183► E S Q S Y L V E D L E R S (SEQ ID NO:5)

661 TCCGGTCAGCCCCTGGCAATCCCAACCAATCATCCTGAATCTGATCTTTTTATACACAAT  
AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA (SEQ ID NO:4)  
TATGCTTTTCGGTCAACTT

FIG. 3

Applicant(s): John Bertin

NOVEL MOLECULES OF THE CARD-RELATED PROTEIN  
FAMILY AND USES THEREOF

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

&gt; hCARD5-DNA

740 aa vs.

&gt; mCARD5-DNA

763 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

68.2% identity; Global alignment score: 2377

```

          10          20          30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  ::::::::::: :.: :.  .:.. :::::::::::  :.:
      CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGGTGAC
          10          20          30          40          50          60

          40          50          60          70          80          90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGACGCCATCCTGGATGCGCTGGA
      :: : :  :  : ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      CGCGGCTGCCCCAGCCAGATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
          70          80          90          100         110         120

          100         110         120         130         140         150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCG
      .:.. :.: :  :  : ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      AAACCTGTCAGGGGATGAACCTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
          130         140         150         160         170         180

          160         170         180         190         200         210
inputs CGAGGGCTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
          190         200         210         220         230         240

          220         230         240         250         260         270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCAGCTAAC-GTGC
      ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      TGACAAACTTGTCTAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
          250         260         270         280         290

          280         290         300         310         320         330
inputs TGC GCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  : ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
          300         310         320         330         340         350

          340         350         360         370         380         390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCTGCG
      ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:.. ::::::::::: :.: :.  .:..
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
          360         370         380         390         400         410

          400         410         420         430         440         450

```

FIG. 5A

FIG. 5B

Applicant(s): John Bertin

NOVEL MOLECULES OF THE CARD-RELATED PROTEIN  
FAMILY AND USES THEREOF

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

&gt; hCARD5-protein 195 aa vs.

&gt; mCARD5-protein 193 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSY
      10      20      30      40      50      60

      70      80      90      100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSAAAPAGIQAPPQSAAKPGLHFIQDQHRA
      .... : : ..... : : : : ..... : ..... : .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90      100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      ..... : : ..... : ..... : ..... : ..... : .....
      ALIARVTEVDGVLDAHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTCDSLLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS (SEQ ID NO:5)
      : : : : :
      LKEIHPYLVMDLEQS (SEQ ID NO:2)
      180     190

```

FIG. 6

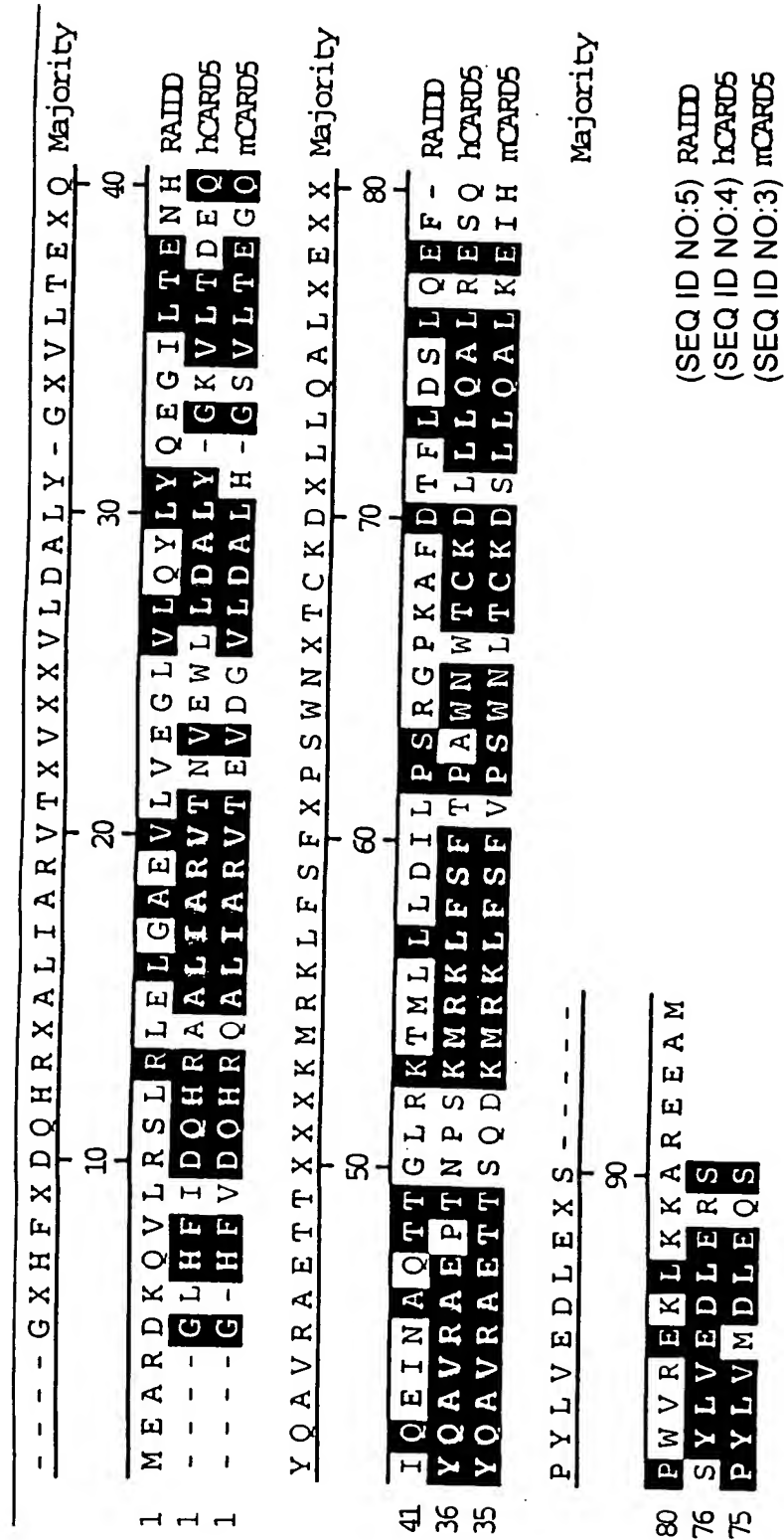


FIG. 7



Applicant(s): John Bertin

NOVEL MOLECULES OF THE CARD-RELATED PROTEIN  
FAMILY AND USES THEREOF

	-	A	-	E	S	-	G	S	E	I	I	D	Q	H	R	X	A	L	L	A	R	V	T	E	D	P	-	D	S	L	L	D	A	L	L	S	R	D	L	I	Majority			
		10		20		30		40																																				
1	I	A	Q	Q	W	-	-	-	-	I	Q	S	K	R	E	D	I	V	N	Q	M	T	E	A	C	L	N	Q	S	L	D	A	L	L	S	R	D	L	I	hCARD3-CARD				
1	-	-	-	-	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	-	Q	C	L	V	D	N	L	L	K	N	D	Y	F	hCARD4-CARD		
1	-	-	-	-	-	-	-	-	-	G	L	H	F	I	D	Q	H	R	A	A	L	I	A	R	V	T	N	-	-	V	E	W	L	L	D	A	L	Y	G	K	-	V	L	hCARD5-CARD
1	-	-	-	-	-	-	-	-	-	G	-	H	F	V	D	O	H	R	Q	A	L	I	A	R	V	T	E	-	-	V	D	G	V	L	D	A	L	H	G	S	-	V	L	hCARD5-CARD
1	M	A	T	E	S	T	P	S	E	I	I	E	R	E	R	K	K	L	L	E	I	L	Q	H	D	P	-	D	S	I	L	D	T	L	T	S	R	R	L	I	hCARD6-CARD			
1	M	A	S	E	G	A	S	S	E	I	I	E	K	Q	R	T	K	L	L	S	V	L	Q	Q	D	P	-	D	S	I	L	D	T	L	T	S	R	R	L	I	hCARD6-CARD			
	S	E	E	D	Y	E	A	V	E	A	E	T	T	X	L	S	K	V	R	K	L	L	I	L	V	Q	S	K	G	E	E	T	C	K	-	F	L	K	C	L	Majority			
		50		60		70		80																																				
36	M	K	E	D	Y	E	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	-	-	-	-	I	A	F	V	I	hCARD3-CARD			
37	S	A	E	D	A	F	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	E	V	S	E	F	F	I	-	Y	L	hCARD4-CARD			
32	T	D	E	Q	Y	Q	A	V	R	A	E	P	T	N	P	S	K	M	R	K	L	F	S	F	T	P	A	W	-	N	W	T	C	K	-	-	-	D	L	L	hCARD5-CARD			
31	T	E	G	Q	Y	Q	A	V	R	A	E	T	S	Q	D	F	M	R	K	L	F	S	F	V	P	S	W	-	N	L	T	C	K	-	-	-	D	S	L	hCARD5-CARD				
40	S	E	E	E	Y	E	T	L	E	N	V	T	D	L	L	K	K	S	R	K	L	L	I	L	V	Q	K	K	G	E	A	T	C	Q	H	F	L	K	C	L	hCARD6-CARD			
40	S	E	E	E	Y	E	T	L	E	A	I	T	D	P	L	K	K	S	R	K	L	L	I	L	I	C	K	K	G	E	D	S	C	C	C	F	L	K	C	L	hCARD6-CARD			
	L	Q	A	L	K	D	S	A	A	Y	L	G	L	D	P	E	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Majority				
		90		100																																								
72	V	Q	K	L	K	D	N	K	Q	-	M	G	L	Q	P	Y	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:10) hCARD3-CARD				
76	L	Q	Q	L	A	F	-	-	-	A	Y	V	D	L	R	P	W	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:11) hCARD4-CARD				
68	L	Q	A	L	R	E	S	Q	S	Y	L	V	E	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:8) hCARD5-CARD					
67	L	Q	A	L	K	E	I	H	P	Y	L	V	M	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:7) hCARD5-CARD					
80	F	S	T	F	P	Q	L	A	I	C	G	L	R	H	E	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:13) hCARD6-CARD					
80	S	N	A	F	P	Q	S	A	S	T	L	G	L	K	Q	E	V	P	R	Q	G	T	G	E	V	F	V	S	-	-	-	-	-	-	-	-	-	-	(SEQ ID NO:14) hCARD6-CARD					

FIG. 8